

SEQUENCE LISTING

<110> Cahoon, Edgar B.
Cahoon, Rebecca E.

<120> Enzymes Involved In Petroselinic Acid Biosynthesis

<130> BB1413 US NA

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<150> 60/169,968
<151> 9 DECEMBER 1999

<160> 12

<170> Microsoft Office 97

<210> 1
<211> 1344
<212> DNA
<213> Hedera helix

<220>
<221> unsure
<222> (997)

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gagcaagatgc gggagttgag ggaagggccc aaggagattc ccgacgacta ttttgtgttg 420
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tggattttca atcgggagtt gaagatatga acaggaaggg aaggggaatg aggagcaaat 1260
gagtgtagta gatttctata tgcattgitta tatattatga atgattatta tataataata 1320
agtgtttgag ttttaagtaa aaaa 1344

<210> 2
<211> 394
<212> PRT
<213> Hedera helix

<220>
<221> UNSURE
<222> (318)

09732597.120800

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          20          25          30

Phe Met Ala Ser Thr Val Asn Ser Asn Ser Met Val Leu Asp Asn Leu
          35          40          45

Lys Ser Pro Pro Asn Leu Gln Val Thr His Ser Met Pro Pro Gln Lys
          50          55          60

Leu Glu Ile Phe Lys Ser Leu Asp Asp Trp Ala Arg Asn Asn Val Leu
          65          70          75          80

Ile His Leu Lys Ser Val Glu Lys Ser Trp Gln Pro Gln Asp Tyr Leu
          85          90          95

Pro Asp Pro Val Ser Asp Gly Phe Glu Glu Gln Val Arg Glu Leu Arg
          100          105          110

Glu Arg Ala Lys Glu Ile Pro Asp Asp Tyr Phe Val Val Leu Val Gly
          115          120          125

Asp Met Ile Thr Glu Glu Ala Leu Pro Thr Tyr Met Ser Met Leu Asn
          130          135          140

Arg Cys Asp Gly Ile Lys Asp Glu Thr Gly Ala Glu Pro Ser Ala Trp
          145          150          155          160

Ala Met Trp Thr Arg Ala Trp Thr Ala Glu Asn Arg His Gly Asp
          165          170          175

Leu Leu Asn Lys Tyr Leu Tyr Leu Ser Gly Arg Val Asp Met Arg Lys
          180          185          190

Ile Glu Lys Thr Ile Gln Tyr Leu Ile Gly Ser Gly Met Asp Ile Lys
          195          200          205

Ser Glu Asn Ser Pro Tyr Leu Gly Phe Ile Tyr Thr Ser Phe Gln Glu
          210          215          220

Arg Ala Thr Phe Ile Ser His Ala Asn Thr Ala Lys Leu Ala Gln His
          225          230          235          240

Tyr Gly Asp Lys Asn Leu Ala His Ile Cys Gly Ser Ile Ala Ser Asp
          245          250          255

Glu Lys Arg His Ala Thr Ala Tyr Thr Lys Ile Val Glu Lys Leu Ala
          260          265          270

Glu Ile Asp Pro Asp Thr Thr Val Ile Ala Phe Ala Asp Met Met Arg
          275          280          285

Lys Lys Ile Thr Met Pro Ala His Leu Met Tyr Asp Gly Ser Asp Glu
          290          295          300

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Leu Leu Phe Lys His Phe Thr Ala Val Ala Gln Arg Val Xaa Val Tyr
305 310 315 320

Ser Ala Leu Asp Tyr Cys Asp Ile Leu Glu Phe Leu Val Asp Lys Trp
325 330 335

Asn Val Glu Arg Leu Thr Gly Leu Ser Asp Glu Gly Arg Lys Ala Gln
340 345 350

Glu Tyr Val Cys Glu Leu Gly Pro Lys Ile Arg Arg Val Glu Glu Lys
355 360 365

Val Gln Gly Lys Glu Lys Lys Lys Ala Glu His Pro Val Ser Phe
370 375 380

Ser Trp Ile Phe Asn Arg Glu Leu Lys Ile
385 390

<210> 3
<211> 445
<212> DNA
<213> Hedera helix

<400> 3
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gttcaatttc actctctgtc aatgggaaat ccttcggttc acttaggttg ctgtcggcac 240
cacttcgctt cagagtgtca tgcgcagcga aaccagcgac agtggacaag gtgtgtgaga 300
ttgtgcggaa acaactggcg ctgcgctga ttctgcaagt cactggagag tcaaaattcg 360
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tcgggaatcaa gcgtgggaaa aagaa 445

<210> 4
<211> 114
<212> PRT
<213> Hedera helix

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20 25 30
Val Asn Gly Lys Ser Phe Arg Ser Leu Arg Leu Leu Ser Ala Pro Leu
35 40 45
Arg Phe Arg Val Ser Cys Ala Ala Lys Pro Ala Thr Val Asp Lys Val
50 55 60
Cys Glu Ile Val Arg Lys Gln Leu Ala Leu Pro Leu Ile Leu Gln Val
65 70 75 80
Thr Gly Glu Ser Lys Phe Ala Ala Leu Gly Ala Asp Ser Leu Asp Thr
85 90 95
Val Glu Ile Val Met Gly Leu Lys Glu Glu Phe Gly Ile Lys Arg Gly
100 105 110

Lys Lys
114

<210> 5
<211> 920
<212> DNA
<213> Hedera helix

<400> 5
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catcgatttc cttcacctct atcgcaagct cctccaagca aaaccaggga cttgccaaaga 180
gttcaatttc actctctgtc aatgggaaat ccttcogttc acttaggttg ctgtcgccac 240
cacttcgctt cagagtgtca tgcgcagcga aaccagcgac agtggaacag gtgtgtgaga 300
ttgtgcggaa acaactggcg ctgccggctg attctgcagt cactggagag tcaaaattcg 360
cagcgcttgg ggtgattct ctgcacacgg ttgagattgt gatgggacta gaggaggaat 420
tcggaatcag cgtggaagaa gaaagtgcac agaccattgc cactgttcaa gatgcagcgg 480
acctgattga gaagcttggt gaaaaaaagg agtagaagaa ccggggtaga aattctgcaa 540
aatagggtta ttaaggacag ttactttatt aggatggttc atcaagatct tcattaccct 600
acattttatt gtatgctcct catgaagccg caaaagttag agtggtgatg aaatttacc 660
cgagtcttcg cottaattat caaagtgaga gagccagaaa aagaggctat gctatctctc 720
atctcgttat gttttatttt cttgtcggac ttctgggttg agtttttttt ttttatctaa 780
acatgatatt agtcttggtt aaaaagtitt caaaaaaata tatcttggtg ttgagactga 840
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<210> 6
<211> 137
<212> PRT
<213> Hedera helix

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20 25 30
Val Asn Gly Lys Ser Phe Arg Ser Leu Arg Leu Leu Ser Ala Pro Leu
35 40 45
Arg Phe Arg Val Ser Cys Ala Ala Lys Pro Ala Thr Val Asp Lys Val
50 55 60
Cys Glu Ile Val Arg Lys Gln Leu Ala Leu Pro Ala Asp Ser Ala Val
65 70 75 80
Thr Gly Glu Ser Lys Phe Ala Ala Leu Gly Ala Asp Ser Leu Asp Thr
85 90 95
Val Glu Ile Val Met Gly Leu Glu Glu Glu Phe Gly Ile Ser Val Glu
100 105 110
Glu Glu Ser Ala Gln Thr Ile Ala Thr Val Gln Asp Ala Ala Asp Leu
115 120 125
Ile Glu Lys Leu Val Glu Lys Lys Glu
130 135

<210> 7
 <211> 385
 <212> PRT
 <213> Coriandrum sativum

<400> 7
 Met Ala Met Lys Leu Asn Ala Leu Met Thr Leu Gln Cys Pro Lys Arg
 1 5 10 15
 Asn Met Phe Thr Arg Ile Ala Pro Pro Gln Ala Gly Arg Val Arg Ser
 20 25 30
 Lys Val Ser Met Ala Ser Thr Leu His Ala Ser Pro Leu Val Phe Asp
 35 40 45
 Lys Leu Lys Ala Gly Arg Pro Glu Val Asp Glu Leu Phe Asn Ser Leu
 50 55 60
 Glu Gly Trp Ala Arg Asp Asn Ile Leu Val His Leu Lys Ser Val Glu
 65 70 75 80
 Asn Ser Trp Gln Pro Gln Asp Tyr Leu Pro Asp Pro Thr Ser Asp Ala
 85 90 95
 Phe Glu Asp Gln Val Lys Glu Met Arg Glu Arg Ala Lys Asp Ile Pro
 100 105 110
 Asp Glu Tyr Phe Val Val Leu Val Gly Asp Met Ile Thr Glu Glu Ala
 115 120 125
 Leu Pro Thr Tyr Met Ser Met Leu Asn Arg Cys Asp Gly Ile Lys Asp
 130 135 140
 Asp Thr Gly Ala Gln Pro Thr Ser Trp Ala Thr Trp Thr Arg Ala Trp
 145 150 155 160
 Thr Ala Glu Glu Asn Arg His Gly Asp Leu Leu Asn Lys Tyr Leu Tyr
 165 170 175
 Leu Ser Gly Arg Val Asp Met Arg Met Ile Glu Lys Thr Ile Gln Tyr
 180 185 190
 Leu Ile Gly Ser Gly Met Asp Thr Lys Thr Glu Asn Cys Pro Tyr Met
 195 200 205
 Gly Phe Ile Tyr Thr Ser Phe Gln Glu Arg Ala Thr Phe Ile Ser His
 210 215 220
 Ala Asn Thr Ala Lys Leu Ala Gln His Tyr Gly Asp Lys Asn Leu Ala
 225 230 235 240
 Gln Val Cys Gly Asn Ile Ala Ser Asp Glu Lys Arg His Ala Thr Ala
 245 250 255
 Tyr Thr Lys Ile Val Glu Lys Leu Ala Glu Ile Asp Pro Asp Thr Thr
 260 265 270
 Val Ile Ala Phe Ser Asp Met Met Arg Lys Lys Ile Gln Met Pro Ala
 275 280 285

His Ala Met Tyr Asp Gly Ser Asp Asp Met Leu Phe Lys His Phe Thr
290 295 300

Ala Val Ala Gln Gln Ile Gly Val Tyr Ser Ala Trp Asp Tyr Cys Asp
305 310 315 320

Ile Ile Asp Phe Leu Val Asp Lys Trp Asn Val Ala Lys Met Thr Gly
325 330 335

Leu Ser Gly Glu Gly Arg Lys Ala Gln Glu Tyr Val Cys Ser Leu Ala
340 345 350

Ala Lys Ile Arg Arg Val Glu Glu Lys Val Gln Gly Lys Glu Lys Lys
355 360 365

Ala Val Leu Pro Val Ala Phe Ser Trp Ile Phe Asn Arg Gln Ile Ile
370 375 380

Ile
385

<210> 8
<211> 137
<212> PRT
<213> Coriandrum sativum

<400> 8
Met Ala Ala Phe Thr Ala Ser Ser Val Ser Phe Thr Pro Leu Ser Ile
1 5 10 15

Ser Leu Asn Gln Thr Lys Gly Phe Ala Arg Gly Ser Val Ser Ile Pro
20 25 30

Ala Lys Ala Lys Ser Phe Gly Ala Leu Thr Leu Arg Asn Ala Pro Leu
35 40 45

Arg Phe Arg Val Ser Cys Ala Ala Lys Pro Glu Thr Val Glu Lys Val
50 55 60

Cys Glu Ile Val Lys Lys Gln Leu Ala Leu Pro Pro Thr Thr Glu Val
65 70 75 80

Ser Gly Asp Ser Lys Phe Ala Ala Leu Gly Ala Asp Ser Leu Asp Thr
85 90 95

Val Glu Ile Val Met Gly Leu Glu Glu Glu Phe Gly Ile Ser Val Glu
100 105 110

Glu Glu Ser Ala Gln Ala Ile Ala Thr Val Gln Asp Ala Ala Asp Leu
115 120 125

Ile Glu Lys Leu Cys Glu Lys Lys Glu
130 135

<210> 9
<211> 1381
<212> DNA
<213> Hedera helix

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aagaagaacc accctgtctgc gtttgctaag tcaccattac cagtgaccag agttagctct 180
ccaagggttt tcatggcttc cactgtcaac tctaactcca tggttcttga taactcmeta 240
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gagttgaggg aaagggccaa ggagattccc gacgactatt ttgtggtgtt agttggagat 480
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aaggatgaga ctggggctga gcccagtgct tgggcaatgt ggaactagggc atggactgcc 600
gaagagaata gacatggtga ccttctcaat aagtaccttt atttgtctgg aagggttgat 660
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<210> 10

<211> 394

<212> PRT

<213> Hedera helix

<400> 10

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Phe Ala Lys Ser Pro Leu Pro Val Thr Arg Val Ser Ser Pro Arg Val
          20          25          30
Phe Met Ala Ser Thr Val Asn Ser Asn Ser Met Val Leu Asp Asn Leu
          35          40          45
Lys Ser Pro Pro Asn Leu Gln Val Thr His Ser Met Pro Pro Gln Lys
          50          55          60
Leu Glu Ile Phe Lys Ser Leu Asp Asp Trp Ala Arg Asn Asn Val Leu
          65          70          75          80
Ile His Leu Lys Ser Val Glu Lys Ser Trp Gln Pro Gln Asp Tyr Leu
          85          90          95
Pro Asp Pro Val Ser Asp Gly Phe Glu Glu Gln Val Arg Glu Leu Arg
          100          105          110
Glu Arg Ala Lys Glu Ile Pro Asp Asp Tyr Phe Val Val Leu Val Gly
          115          120          125
Asp Met Ile Thr Glu Glu Ala Leu Pro Thr Tyr Met Ser Met Leu Asn
          130          135          140

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Arg Cys Asp Gly Ile Lys Asp Glu Thr Gly Ala Glu Pro Ser Ala Trp
 145 150 155 160
 Ala Met Trp Thr Arg Ala Trp Thr Ala Glu Glu Asn Arg His Gly Asp
 165 170 175
 Leu Leu Asn Lys Tyr Leu Tyr Leu Ser Gly Arg Val Asp Met Arg Lys
 180 185 190
 Ile Glu Lys Thr Ile Gln Tyr Leu Ile Gly Ser Gly Met Asp Ile Lys
 195 200 205
 Ser Glu Asn Ser Pro Tyr Leu Gly Phe Ile Tyr Thr Ser Phe Gln Glu
 210 215 220
 Arg Ala Thr Phe Ile Ser His Ala Asn Thr Ala Lys Leu Ala Gln His
 225 230 235 240
 Tyr Gly Asp Lys Asn Leu Ala His Ile Cys Gly Ser Ile Ala Ser Asp
 245 250 255
 Glu Lys Arg His Ala Thr Ala Tyr Thr Lys Ile Val Glu Lys Leu Ala
 260 265 270
 Glu Ile Asp Pro Asp Thr Thr Val Ile Ala Phe Ala Asp Met Met Arg
 275 280 285
 Lys Lys Ile Thr Met Pro Ala His Leu Met Tyr Asp Gly Ser Asp Glu
 290 295 300
 Leu Leu Phe Lys His Phe Thr Ala Val Ala Gln Arg Val Gly Val Tyr
 305 310 315 320
 Ser Ala Leu Asp Tyr Cys Asp Ile Leu Glu Phe Leu Val Asp Lys Trp
 325 330 335
 Asn Val Glu Arg Leu Thr Gly Leu Ser Asp Glu Gly Arg Lys Ala Gln
 340 345 350
 Glu Tyr Val Cys Glu Leu Gly Pro Lys Ile Arg Arg Val Glu Glu Lys
 355 360 365
 Val Gln Gly Lys Glu Lys Lys Lys Lys Ala Glu His Pro Val Ser Phe
 370 375 380
 Ser Trp Ile Phe Asn Arg Glu Leu Lys Ile
 385 390

<210> 11
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer

<400> 11
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<210> 12
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 12
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27